



1

SEQUENCE LISTING

(1) GENERAL INFORMATION:

(i) APPLICANT: ANDERSON, DARRELL R.
HANNA, NABIL
LEONARD, JOHN E.
NEWMAN, ROLAND A.
REFF, MITCHELL E.
RASTETTER, WILLIAM H.

(ii) TITLE OF INVENTION: THERAPEUTIC APPLICATION OF CHIMERIC AND
RADIOLABELED ANTIBODIES TO HUMAN B LYMPHOCYTE RESTRICTED
DIFFERENTIATION ANTIGEN FOR THE TREATMENT OF B CELL
LYMPHOMA

(iii) NUMBER OF SEQUENCES: 11

(iv) CORRESPONDENCE ADDRESS:

(A) ADDRESSEE: PILLSBURY WINTHROP
(B) STREET: 1100 New York Avenue, N.W., Ninth FL.
(C) CITY: Washington
(D) STATE: DC
(E) COUNTRY: USA
(F) ZIP: 20005

(v) COMPUTER READABLE FORM:

(A) MEDIUM TYPE: Floppy disk
(B) COMPUTER: IBM PC compatible
(C) OPERATING SYSTEM: PC-DOS/MS-DOS
(D) SOFTWARE: PatentIn Release #1.0, Version #1.30

(vi) CURRENT APPLICATION DATA:

(A) APPLICATION NUMBER: US 08/921,060
(B) FILING DATE: 29-AUG-1997
(C) CLASSIFICATION:

(vii) PRIOR APPLICATION DATA:

(A) APPLICATION NUMBER: US 08/149,099
(B) FILING DATE: 03-NOV-1993

(viii) PRIOR APPLICATION DATA:

(A) APPLICATION NUMBER: US 07/978,891
(B) FILING DATE: 13-NOV-1992

(ix) ATTORNEY/AGENT INFORMATION:

(A) NAME: Teskin, Robin L.
(B) REGISTRATION NUMBER: 35,030
(C) REFERENCE/DOCKET NUMBER: 037003-0275463

(x) TELECOMMUNICATION INFORMATION:

(A) TELEPHONE: 202-861-3000
(B) TELEFAX: 202-822-0944

(2) INFORMATION FOR SEQ ID NO:1:

#37
RECEIVED
NOV 23 2001
TECH CENTER 1600/2900

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 27 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

GGGAGCTTGG ATCGATCCTC TATGGTT

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(2) INFORMATION FOR SEQ ID NO:2:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 8540 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

GACGTGCGGG CCGCTCTAGG CCTCCAAAAA AGCCTCCTCA CTACTTCTGG AATAGCTCAG 60
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 ATGGTTGCTG ACTAATTGAG ATGCATGCT TGCACTACTTC TGCTGCTGG GGAGCCTGGG 240
 GACTTTCCAC ACCTGGTTGC TGACTAATTG AGATGCATGC TTTGCATACT TCTGCCTGCT 300
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 CATCACAGAT CTCTCACCAC GAGGGTCCCC GCTCAGCTCC TGGGGCTCCT GCTGCTCTGG 1020
 CTCCCAGGTG CACGATGTGA TGGTACCAAG GTGGAAATCA AACGTACGGT GGCTGCACCA 1080
 TCTGTCTTCA TCTTCCCGCC ATCTGATGAG CAGTTGAAAT CTGGAACTGC CTCCTGTTGT 1140
 TGCCTGCTGA ATAACCTCTA TCCCAGAGAG GCCAAAGTAC AGTGGAAAGGT GGATAACGCC 1200
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 AGTGGTGGCC TAACTACGGC TACACTAGAA GGACAGTATT TGGTATCTGC GCTCTGCTG 7260
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 CCCAACGATC AAGGCGAGTT ACATGATCCC CCATGTTGTG CAAAAAAAGCG GTTAGCTCCT 7980
 TCGGTCTTCC GATCGTTGTC AGAAGTAAGT TGGCCGCAGT GTTATCACTC ATGGTTATGG 8040
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 AACCCACTCG TGCACCCAAAC TGATCTTCAG CATCTTTAC TTTCACCGC GTTGTGGGT 8340
 GAGCAAAAC AGGAAGGCAA AATGCCGCAA AAAAGGGAAT AAGGGCGACA CGGAAATGTT 8400
 GAATACTCAT ACTCTTCCTT TTCAATATT ATTGAAGCAT TTATCAGGGT TATTGTCTCA 8460
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 TTCCCCGAAA AGTGCCACCT 8540

(2) INFORMATION FOR SEQ ID NO:3:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 9209 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

GACGTCGCGG	CCGCTCTAGG	CCTCCAAAAA	AGCCTCCTCA	CTACTTCTGG	AATAGCTCAG	60
AGGCCGAGGC	GGCCTCGGCC	TCTGCATAAA	TAAAAAAAAT	TAGTCAGCCA	TGCATGGGGC	120
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ATGGTTGCTG	ACTAATTGAG	ATGCATGCTT	TGCATACTTC	TGCCTGCTGG	GGAGCCTGGG	240
GACTTTCCAC	ACCTGGTTGC	TGACTAATTG	AGATGCATGC	TTTGCTACT	TCTGCCTGCT	300
GGGGAGCCTG	GGGACTTTCC	ACACCCTAAC	TGACACACAT	TCCACAGAAT	TAATTCCCCT	360
AGTTATTAAT	AGTAATCAAT	TACGGGGTCA	TTAGTTCAT	GCCCCATATAT	GGAGTTCCGC	420
GTTACATAAC	TTACGGTAAA	TGGCCCGCCT	GGCTGACCGC	CCAACGACCC	CCGCCCATTG	480
ACGTCAATAA	TGACGTATGT	TCCCATAGTA	ACGCCAATAG	GGACTTCCA	TTGACGTCAA	540
TGGGTGGACT	ATTACGGTA	AACTGCCAC	TTGGCAGTAC	ATCAAGTGT	TCATATGCCA	600
AGTACGCC	CTATTGACGT	CAATGACGGT	AAATGGCCCG	CCTGGCATT	TGCCCAGTAC	660
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GACTTTCCAA	AATGTGTA	CAACTCCGCC	CCATTGACGC	AAATGGCGG	TAGGC GTGTA	900
CGGTGGGAGG	TCTATATAAG	CAGAGCTGGG	TACGTGAACC	GTCAGATCGC	CTGGAGACGC	960
CATCACAGAT	CTCTCACTAT	GGATTTTCAG	GTGCAGATTA	TCAGCTCCT	GCTAATCAGT	1020
GCTTCAGTCA	TAATGTCCAG	AGGACAATT	GTTCCTCTCCC	AGTCTCCAGC	AATCCTGTCT	1080
GCATCTCCAG	GGGAGAAGGT	CACAATGACT	TGCAGGGCCA	GCTCAAGTGT	AAGTTACATC	1140
CACTGGTTCC	AGCAGAACGCC	AGGATCCTCC	CCCAAACCCCT	GGATTTATGC	CACATCCAAC	1200
CTGGCTTCTG	GAGTCCCTGT	TCGCTTCAGT	GGCAGTGGGT	CTGGGACTTC	TTACTCTCTC	1260
ACAATCAGCA	GAGTGGAGGC	TGAAGATGCT	GCCACTTATT	ACTGCCAGCA	GTGGACTAGT	1320
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TCTGTCTTCA	TCTTCCCGCC	ATCTGATGAG	CAGTGAAAT	CTGGAACTGC	CTCTGTTGTG	1440
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TGTTGAATTC	AGATCCGTTA	ACGGTTACCA	ACTACCTAGA	CTGGATTCTG	GACAACATGC	1740
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GTTCGCCCT	CCCCCGTGC	TTCCCTGACC	CTGGAAGGTG	CCACTCCCAC	TGTCCTTTCC	1860
TAATAAAATG	AGGAAATTGC	ATCGCATTGT	CTGAGTAGGT	GTCATTCTAT	TCTGGGGGGT	1920
GGGGTGGGGC	AGGACAGCAA	GGGGGAGGAT	TGGGAAGACA	ATAGCAGGCA	TGCTGGGGAT	1980
GCGGTGGGCT	CTATGGAACC	AGCTGGGCT	CGACAGCTAT	GCCAAGTACG	CCCCCTATTG	2040
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TACATCTGCA	ACGTGAATCA	CAAGCCCAGC	AACACCAAGG	TGGACAAGAA	AGCAGAGCCC	3120
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CAGAAGAGCC	TCTCCCTGTC	TCCGGTAAA	TGAGGATCCG	TTAACGGTTA	CCAACATACCT	3840
AGACTGGATT	CGTGACAACA	TGCGGCGGTG	ATATCTACGT	ATGATCAGCC	TCGACTGTGC	3900
CTTCTAGTTG	CCAGCCATCT	GTTGTTGCC	CCTCCCCCGT	GCCTTCCTTG	ACCCCTGGAAG	3960
GTGCCACTCC	CACTGTCCTT	TCCTAATAAA	ATGAGGAAAT	TGCATCGCAT	TGTCAGTA	4020
GGTGTCAATT	TATTCTGGGG	GGTGGGGTGG	GGCAGGACAG	CAAGGGGGAG	GATTGGGAAG	4080
ACAATAGCAG	GCATGCTGGG	GATGCGGTGG	GCTCTATGGA	ACCAGCTGGG	GCTCGACAGC	4140
GCTGGATCTC	CCGATCCCCA	GCTTGTCTC	TCAATTCTT	ATTTCGATAA	TGAGAAAAAA	4200
AGGAAAATTA	ATTTTAACAC	CAATTCAAGTA	GTTGATTGAG	CAAATGCGTT	GCCAAAAAAGG	4260
ATGCTTTAGA	GACAGTGTTC	TCTGCACAGA	TAAGGACAA	CATTATTCAAG	AGGGAGTACC	4320
CAGAGCTGAG	ACTCTTAAGC	CAGTGAGTGG	CACAGCATT	TAGGGAGAAA	TATGCTTGT	4380
ATCACCGAAG	CCTGATTCCG	TAGAGCCACA	CCTTGGTAAG	GGCCAATCTG	CTCACACAGG	4440
ATAGAGAGGG	CAGGAGCCAG	GGCAGAGCAT	ATAAGGTGAG	GTAGGATCAG	TTGCTCCTCA	4500
CATTTGCTTC	TGACATAGTT	GTGTTGGAG	CTTGGATAGC	TTGGACAGCT	CAGGGCTGCG	4560
ATTTCGCGCC	AAACTTGACG	GCAATCCTAG	CGTGAAAGGCT	GGTAGGATTT	TATCCCCGCT	4620
GCCATCATGG	TTCGACCATT	GAACTGCATC	GTGCCCGTGT	CCCAAAATAT	GGGGATTGGC	4680
AAGAACGGAG	ACCTACCTG	GCCTCCGCTC	AGGAACGAGT	TCAAGTACTT	CCAAAGAATG	4740
ACCACAAACCT	CTTCAGTGGA	AGGTAAACAG	AATCTGGTGA	TTATGGTAG	GAAAACCTGG	4800
TTCTCCATTC	CTGAGAAGAA	TCGACCTTTA	AAGGACAGAA	TTAATATAGT	TCTCAGTAGA	4860
GAACCTCAAAG	AACCACCACG	AGGAGCTCAT	TTTCTTGCCA	AAAGTTGGA	TGATGCCCTA	4920
AGACTTATTG	AACAACCGGA	ATTGGCAAGT	AAAGTAGACA	TGGTTGGAT	AGTCGGAGGC	4980
AGTTCTGTT	ACCAAGGAAGC	CATGAATCAA	CCAGGCCACC	TTAGACTCTT	TGTGACAAGG	5040
ATCATGCAGG	AATTGAAAG	TGACACGTTT	TTCCCAGAAA	TTGATTGGG	GAAATATAAA	5100
CTTCTCCCGAG	AATACCCAGG	CGTCCTCTCT	GAGGTCCAGG	AGGAAAAAAGG	CATCAAGTAT	5160
AAGTTTGAAG	TCTACGAGAA	GAAAGACTAA	CAGGAAGATG	CTTTCAAGTT	CTCTGCTCCC	5220
CTCCTAAAGC	TATGCATT	TATAAGACCA	TGGGACTTTT	GCTGGCTTTA	GATCAGCCTC	5280
GAAGTGTGCT	TCTAGTTGCC	AGCCATCTGT	TGTTTGCCCC	TCCCCCGTGC	CTTCCTTGAC	5340
CCTGGAAAGGT	GCCACTCCCCA	CTGTCTTTC	CTAATAAAAT	GAGGAATTG	CATCGCATTG	5400
TCTGAGTAGG	TGTCTTCTA	TTCTGGGGGG	TGGGGTGGGG	CAGGACAGCA	AGGGGGAGGA	5460
TTGGGAAGAC	AATAGCAGGC	ATGCTGGGGA	TGCGGTGGGC	TCTATGGAAC	CAGCTGGGGC	5520
TCGAGCTACT	AGCTTTGCTT	CTCAATTCT	TATTTCGATA	ATGAGAAAAA	AAGGAAAATT	5580
AATTTAACAA	CCAATTCAAGT	AGTTGATTGA	GCAAATGCGT	TGCCAAAAG	GATGCTTTAG	5640
AGACAGTGT	CTCTGCACAG	ATAAGGACAA	ACATTATTCA	GAGGGAGTAC	CCAGAGCTGA	5700
GACTCCTAAG	CCAGTGAGTC	GCACAGCATT	CTAGGGAGAA	ATATGCTTGT	CATCACCGAA	5760
GCCTGATTCC	GTAGAGCCAC	ACCTTGGTAA	GGGCCAATCT	GCTCACACAG	GATAGAGAGG	5820
GCAGGAGCCA	GGGCAGAGCA	TATAAGGTGA	GGTAGGATCA	GTGCTCCTC	ACATTGCTT	5880
CTGACATAGT	TGTGTTGGGA	GCTTGGATCG	ATCCTCTATG	GTTGAACAAG	ATGGATTGCA	5940
CGCAGGTTCT	CCGGCCGCTT	GGGTGGAGAG	GCTATTGGC	TATGACTGGG	CACAAACAGAC	6000
AATCGGCTGC	TCTGATGCCG	CCGTGTTCCG	GCTGTAGCG	CAGGGCGGCC	CGGTTCTTTT	6060

TGTCAAGACC	GACCTGTCCG	GTGCCCTGAA	TGAAC TGCA G	GACGAGGCAG	CGCGGCTATC	6120
GTGGCTGGCC	ACGACGGCG	TTCC TTGCGC	AGCTGTGCTC	GACGTTGTCA	CTGAAGCGGG	6180
AAGGGACTGG	CTGCTATTGG	GCGAAGTGCC	GGGGCAGGAT	CTCCTGTCAT	CTCACCTTGC	6240
TCCTGCCAG	AAAGTATCCA	TCATGGCTGA	TGCAATGC GG	CGGCTGCATA	CGCTTGATCC	6300
GGCTACCTGC	CCATTGAC	ACCAAGCGA	ACATCGCATC	GAGCGAGCAC	GTACTCGGAT	6360
GGAAGCCGGT	CTTGTGATC	AGGATGATCT	GGACGAAGAG	CATCAGGGC	TCGCGCCAGC	6420
CGAACTGTT	GCCAGGCTCA	AGGC GCGCAT	GCCC GACGGC	GAGGATCTCG	TCGTGACCCA	6480
TGGCGATGCC	TGCTTGCCGA	ATATCATGGT	GGAAAATGGC	CGCTTTCTG	GATT CATCGA	6540
CTGTGGCCGG	CTGGGTGTGG	CGGACCGCTA	TCAGGACATA	GCGTTGGCTA	CCCGTGATAT	6600
TGCTGAAGAG	CTTGGCGGCG	AATGGGCTGA	CCGCTTCC	GTGCTTTACG	GTATCGCCGC	6660
TCCC GATTG	CAGCGCATCG	CCTTCTATCG	CCTTCTGAC	GAGTTCTTCT	GAGCGGGACT	6720
CTGGGGTTCG	AAATGACCGA	CCAAGCGACG	CCCAACCTGC	CATCACCGA	TTTCGATTCC	6780
ACCGCCGCCT	TCTATGAAAG	GTTGGGCTTC	GGAAATCGTT	TCCGGGACGC	CGGCTGGATG	6840
ATCCTCCAGC	GCGGGGATCT	CATGCTGGAG	TTCTCGCC	ACCCCAACTT	GTTTATTGCA	6900
GCTTATAATG	GTTACAAATA	AAGCAATAGC	ATCACAAATT	TCACAAATAA	AGCATTTTT	6960
TCACTGCATT	CTAGTTGTGG	TTTGTCCAAA	CTCATCAATC	TATCTTATCA	TGCTGGATC	7020
GCGGCCGCGA	TCCCCGCGAG	AGCTTGGCGT	AATCATGGTC	ATAGCTGTTT	CCTGTGTGAA	7080
ATTGTTATCC	GCTCACAAATT	CCACACAAACA	TACGAGGCCG	AAGCATAAAG	TGAAAGCCT	7140
GGGGTGCCTA	ATGAGTGAGC	TAACTCACAT	TAATTGCGTT	GCGCTCACTG	CCCGCTTTCC	7200
AGTCGGGAAA	CCTGTCGTG	CAGCTGCATT	AATGAATCGG	CCAACCGCG	GGGAGAGGCG	7260
GT T T G C G T A T	TGGCGCTCT	TCCGCTTCC	CGCTCACTGA	CTCGCTGC	T CG GT CG TT	7320
GGCTGCGGCG	AGCGGTATCA	GCTCACTCAA	AGGCGGTAA	ACGGTTATCC	ACAGAATCAG	7380
GGGATAACGC	AGGAAAGAAC	ATGTGAGCA	AAGGCCAGCA	AAAGGCCAGG	AAACGTAAAA	7440
AGGCCGCGTT	GCTGGCGTTT	TTCCATAGGC	TCCGCC	TGACGAGCAT	CACAAAATC	7500
GACGCTCAAG	TCAGAGGTGG	CGAAACCCGA	CAGGACTATA	AAGATACCA	CGTTTCCCC	7560
CTGGAAGCTC	CCTCGTGC	TCTCCTGTT	CGACCC	GCTTACCGA	TACCTGTCCG	7620
CCTTTCTCCC	TTCGGGAA	GTGGCGCTT	CTCAATGCTC	ACGCTGTAGG	TATCTCAGTT	7680
CGGTGTAGGT	CGTTGCTCC	AAGCTGGCT	GTGTGCACGA	ACCCCCGTT	CAGCCGACC	7740
GCTGCGCTT	ATCCGTAAC	TATCGTCTG	AGTCCAACCC	GGTAAGACAC	GACTTATCGC	7800
CACTGGCAGC	AGCCACTGGT	AA CAGGATTA	GCAGAGCGAG	GTATGTAGGC	GGTGTACAG	7860
AGTTCTTGA	GTGGTGGCCT	AACTACGGCT	ACACTAGAAG	GACAGTATT	GGTATCTGCG	7920
CTCTGCTGAA	GCCAGTTACC	TTCGGAAAAA	GAGTTGGTAG	CTCTTGATCC	GGCAAACAAA	7980
CCACCGCTGG	TAGCGGTGGT	TTTTTGTTT	GCAAGCAGCA	GATTACCGC	AGAAAAAAAG	8040
GATCTCAAGA	AGATCCTTTG	ATCTTTCTA	CGGGGTCTGA	CGCTCAGTGG	AA CG AAA ACT	8100
CACGTTAAGG	GATTGGTC	ATGAGATTAT	CAAAAAGGAT	CTTCACCTAG	ATCCTTTAA	8160
ATTAAAAATG	AAGTTTTAAA	TCAATCTAA	GTATATATGA	GTAAACTTGG	TCTGACAGTT	8220
ACCAATGCTT	AATCAGTGAG	GCACCTATCT	CAGCGATCTG	TCTATTTCTG	TCATCCATAG	8280
TTGCTGACT	CCCCGTCGT	TAGATAACTA	CGATA CGGG	GGGCTTACCA	TCTGGCCCCA	8340
GTGCTGCAAT	GATACCGCGA	GACCCACGCT	CACCGGCTCC	AGATTATATCA	GCAATAAAC	8400
AGCCAGCCGG	AAGGGCGAG	CGCAGAAGTG	GTCC	TCCATCCAGT	8460	
CTATTAAATTG	TTGCCGGAA	GCTAGAGTAA	GTAGTTG	AGTTAATAGT	TTGCCAACG	8520
TTGTTGCCAT	TGCTACAGGC	ATCGTGGTGT	CACGCTCGTC	GTTTGGTATG	GCTTCATTCA	8580
GCTCCGGTTC	CCAACGATCA	AGGC GAGTTA	CATGATCCC	CATGTTGTG	AAAAAAGCGG	8640
TTAGCTCCCT	CGGTCTCCG	ATCGTTGTCA	GAAGTAAGTT	GGCCG	TTATCACTCA	8700
TGGTTATGGC	AGCACTGCAT	AATTCTT	CTGTCATG	ATCCGTAAGA	TGCTTTCTG	8760
TGACTGGTGA	GTACTCAACC	AAGTCATTCT	GAGAATAGTG	TATGCGGCGA	CCGAGTTGCT	8820
CTTGCCCGGC	GTCAATACGG	GATAATACCG	CGCCACATAG	CAGAACTTTA	AAAGTGCTCA	8880
TCATTGGAAA	ACGTTCTCG	GGGC	TCTCAAGGAT	CTTACCGCTG	TTGAGATCCA	8940
GTTCGATGTA	ACCCACTCGT	GCACCCAACT	GATCTTCAGC	ATCTTTACT	TTCACCA	9000
TTTCTGGGTG	AGCAAAAACA	GGAAAGGCAA	ATGCGCAA	AAAGGAAATA	AGGGCGACAC	9060
GGAAATGTTG	AATACTCAT	CTCTT	TTCAATATTA	TTGAAGCATT	TATCAGGGTT	9120
ATTGTCTCAT	GAGCGGATAC	ATATTG	GTATTGAA	AAATAACAA	ATAGGGGTT	9180
CGCGCACATT	TCCCCGAAAA	GTGCCACCT				9209

(2) INFORMATION FOR SEQ ID NO:4:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 47 base pairs

- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

ATCACAGATC TCTCACCAGT GATTTTCAGG TGCAGATTAT CAGCTTC

47

(2) INFORMATION FOR SEQ ID NO:5:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 30 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid
 (A) DESCRIPTION: /desc = "primer"

(iv) ANTI-SENSE: YES

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:

TGCAGCATCC GTACGTTGA TTTCCAGCTT

30

(2) INFORMATION FOR SEQ ID NO:6:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 384 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 1..384

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:

ATG GAT TTT CAG GTG CAG ATT ATC AGC TTC CTG CTA ATC AGT GCT TCA
 Met Asp Phe Gln Val Gln Ile Ile Ser Phe Leu Leu Ile Ser Ala Ser
 1 5 10 15

48

GTC ATA ATG TCC AGA GGG CAA ATT GTT CTC TCC CAG TCT CCA GCA ATC
 Val Ile Met Ser Arg Gly Gln Ile Val Leu Ser Gln Ser Pro Ala Ile
 20 25 30

96

CTG TCT GCA TCT CCA GGG GAG AAG GTC ACA ATG ACT TGC AGG GCC AGC Leu Ser Ala Ser Pro Gly Glu Lys Val Thr Met Thr Cys Arg Ala Ser 35 40 45	144
TCA AGT GTA AGT TAC ATC CAC TGG TTC CAG CAG AAG CCA GGA TCC TCC Ser Ser Val Ser Tyr Ile His Trp Phe Gln Gln Lys Pro Gly Ser Ser 50 55 60	192
CCC AAA CCC TGG ATT TAT GCC ACA TCC AAC CTG GCT TCT GGA GTC CCT Pro Lys Pro Trp Ile Tyr Ala Thr Ser Asn Leu Ala Ser Gly Val Pro 65 70 75 80	240
GTT CGC TTC AGT GGC AGT GGG TCT GGG ACT TCT TAC TCT CTC ACA ATC Val Arg Phe Ser Gly Ser Gly Thr Ser Tyr Ser Leu Thr Ile 85 90 95	288
AGC AGA GTG GAG GCT GAA GAT GCT GCC ACT TAT TAC TGC CAG CAG TGG Ser Arg Val Glu Ala Glu Asp Ala Ala Thr Tyr Tyr Cys Gln Gln Trp 100 105 110	336
ACT AGT AAC CCA CCC ACG TTC GGA GGG GGG ACC AAG CTG GAA ATC AAA Thr Ser Asn Pro Pro Thr Phe Gly Gly Thr Lys Leu Glu Ile Lys 115 120 125	384

(2) INFORMATION FOR SEQ ID NO:7:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 128 amino acids
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:7:

Met Asp Phe Gln Val Gln Ile Ile Ser Phe Leu Leu Ile Ser Ala Ser 1 5 10 15	
Val Ile Met Ser Arg Gly Gln Ile Val Leu Ser Gln Ser Pro Ala Ile 20 25 30	
Leu Ser Ala Ser Pro Gly Glu Lys Val Thr Met Thr Cys Arg Ala Ser 35 40 45	
Ser Ser Val Ser Tyr Ile His Trp Phe Gln Gln Lys Pro Gly Ser Ser 50 55 60	
Pro Lys Pro Trp Ile Tyr Ala Thr Ser Asn Leu Ala Ser Gly Val Pro 65 70 75 80	
Val Arg Phe Ser Gly Ser Gly Thr Ser Tyr Ser Leu Thr Ile 85 90 95	
Ser Arg Val Glu Ala Glu Asp Ala Ala Thr Tyr Tyr Cys Gln Gln Trp 100 105 110	

Thr Ser Asn Pro Pro Thr Phe Gly Gly Gly Thr Lys Leu Glu Ile Lys
 115 120 125

(2) INFORMATION FOR SEQ ID NO:8:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 27 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:8:

GCGGCTCCCA CGCGTGTCT GTCCAG

27

(2) INFORMATION FOR SEQ ID NO:9:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 29 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid
 (A) DESCRIPTION: /desc = "primer"

(iv) ANTI-SENSE: YES

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:9:

GGSTGTTGTG CTAGCTGMRG AGACRG TG A

29

(2) INFORMATION FOR SEQ ID NO:10:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 420 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 1..420

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:10:

ATG GGT TGG AGC CTC ATC TTG CTC TTC CTT GTC GCT GTT GCT ACG CGT Met Gly Trp Ser Leu Ile Leu Leu Phe Leu Val Ala Val Ala Thr Arg 1 5 10 15	48
GTC CTG TCC CAG GTA CAA CTG CAG CAG CCT GGG GCT GAG CTG GTG AAG Val Leu Ser Gln Val Gln Leu Gln Pro Gly Ala Glu Leu Val Lys 20 25 30	96
CCT GGG GCC TCA GTG AAG ATG TCC TGC AAG GCT TCT GGC TAC ACA TTT Pro Gly Ala Ser Val Lys Met Ser Cys Lys Ala Ser Gly Tyr Thr Phe 35 40 45	144
ACC AGT TAC AAT ATG CAC TGG GTA AAA CAG ACA CCT GGT CGG GGC CTG Thr Ser Tyr Asn Met His Trp Val Lys Gln Thr Pro Gly Arg Gly Leu 50 55 60	192
GAA TGG ATT GGA GCT ATT TAT CCC GGA AAT GGT GAT ACT TCC TAC AAT Glu Trp Ile Gly Ala Ile Tyr Pro Gly Asn Gly Asp Thr Ser Tyr Asn 65 70 75 80	240
CAG AAG TTC AAA GGC AAG GCC ACA TTG ACT GCA GAC AAA TCC TCC AGC Gln Lys Phe Lys Gly Lys Ala Thr Leu Thr Ala Asp Lys Ser Ser Ser 85 90 95	288
ACA GCC TAC ATG CAG CTC AGC AGC CTG ACA TCT GAG GAC TCT GCG GTC Thr Ala Tyr Met Gln Leu Ser Ser Leu Thr Ser Glu Asp Ser Ala Val 100 105 110	336
TAT TAC TGT GCA AGA TCG ACT TAC TAC GGC GGT GAC TGG TAC TTC AAT Tyr Tyr Cys Ala Arg Ser Thr Tyr Tyr Gly Gly Asp Trp Tyr Phe Asn 115 120 125	384
GTC TGG GGC GCA GGG ACC ACG GTC ACC GTC TCT GCA Val Trp Gly Ala Gly Thr Thr Val Thr Val Ser Ala 130 135 140	420

(2) INFORMATION FOR SEQ ID NO:11:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 140 amino acids
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:11:

Met Gly Trp Ser Leu Ile Leu Leu Phe Leu Val Ala Val Ala Thr Arg 1 5 10 15
Val Leu Ser Gln Val Gln Leu Gln Gln Pro Gly Ala Glu Leu Val Lys 20 25 30
Pro Gly Ala Ser Val Lys Met Ser Cys Lys Ala Ser Gly Tyr Thr Phe 35 40 45

Thr Ser Tyr Asn Met His Trp Val Lys Gln Thr Pro Gly Arg Gly Leu
50 55 60

Glu Trp Ile Gly Ala Ile Tyr Pro Gly Asn Gly Asp Thr Ser Tyr Asn
65 70 75 80

Gln Lys Phe Lys Gly Lys Ala Thr Leu Thr Ala Asp Lys Ser Ser Ser
85 90 95

Thr Ala Tyr Met Gln Leu Ser Ser Leu Thr Ser Glu Asp Ser Ala Val
100 105 110

Tyr Tyr Cys Ala Arg Ser Thr Tyr Tyr Gly Gly Asp Trp Tyr Phe Asn
115 120 125

Val Trp Gly Ala Gly Thr Thr Val Thr Val Ser Ala
130 135 140